



IFWO

RAW SEQUENCE LISTING DATE: 08/31/2004
 PATENT APPLICATION: US/10/718,933 TIME: 12:19:11

Input Set : N:\Crf3\RULE60\10718933.raw
 Output Set: N:\CRF4\08312004\J718933.raw

1 <110> APPLICANT: Yon, Jeffrey, R
 2 Grantham, Christopher J
 3 Groot-Kormelink, Paulus J
 4 <120> TITLE OF INVENTION: Nicotinic Acetylcholine Receptor
 5 <130> FILE REFERENCE: JAB 1529 USA
 6 <140> CURRENT APPLICATION NUMBER: US/10/718,933
 7 <141> CURRENT FILING DATE: 2003-11-20
 8 <150> PRIOR APPLICATION NUMBER: US/09/661,812
 9 <151> PRIOR FILING DATE: 2000-09-14
 10 <150> PRIOR APPLICATION NUMBER: US 60/153,948
 11 <151> PRIOR FILING DATE: 1999-09-15
 12 <150> PRIOR APPLICATION NUMBER: GB 0002431.5
 13 <151> PRIOR FILING DATE: 2000-02-02
 14 <160> NUMBER OF SEQ ID NOS: 24
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1299
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (1)..(1299)
 24 <400> SEQUENCE: 1
 25 gtg gaa aca gag tgc ctg gga gct gag ggc cgg ctg gct ctc aag ctg 48
 26 Val Glu Thr Glu Cys Leu Gly Ala Glu Gly Arg Leu Ala Leu Lys Leu
 27 1 5 10 15
 28 ttc cgt gac ctc ttt gcc aac tac aca agt gcc ctg aga cct gtg gca 96
 29 Phe Arg Asp Leu Phe Ala Asn Tyr Thr Ser Ala Leu Arg Pro Val Ala
 30 20 25 30
 31 gac aca gac cag act ctg aat gtg acc ctg gag gtg aca ctg tcc cag 144
 32 Asp Thr Asp Gln Thr Leu Asn Val Thr Leu Glu Val Thr Leu Ser Gln
 33 35 40 45
 34 atc atc gac atg gat gaa cgg aac cag gtg ctg acc ctg tat ctg tgg 192
 35 Ile Ile Asp Met Asp Glu Arg Asn Gln Val Leu Thr Leu Tyr Leu Trp
 36 50 55 60
 37 ata cgg cag gag tgg aca gat gcc tac cta cga tgg gac ccc aat gcc 240
 38 Ile Arg Gln Glu Trp Thr Asp Ala Tyr Leu Arg Trp Asp Pro Asn Ala
 39 65 70 75 80
 40 tat ggt ggc ctg gat gcc atc cgc atc ccc agc agt ctt gtg tgg cgg 288
 41 Tyr Gly Leu Asp Ala Ile Arg Ile Pro Ser Ser Leu Val Trp Arg
 42 85 90 95
 43 cca gac atc gta ctc tat aac aaa gcc gac gcg cag cct cca ggt tcc 336
 44 Pro Asp Ile Val Leu Tyr Asn Lys Ala Asp Ala Gln Pro Pro Gly Ser

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45	100	105	110	
46	gcc agc acc aac gtg gtc ctg cgc cac gat ggc gcc gtg cgc tgg gac			384
47	Ala Ser Thr Asn Val Val Leu Arg His Asp Gly Ala Val Arg Trp Asp			
48	115	120	125	
49	gcg ccg gcc atc acg cgc agc tcg tgc cgc gtg gat gta gca gcc ttc			432
50	Ala Pro Ala Ile Thr Arg Ser Ser Cys Arg Val Asp Val Ala Ala Phe			
51	130	135	140	
52	ccg ttc gac gcc cag cac tgc ggc ctg acg ttc ggc tcc tgg act cac			480
53	Pro Phe Asp Ala Gln His Cys Gly Leu Thr Phe Gly Ser Trp Thr His			
54	145	150	155	160
55	ggc ggg cac caa ctg gat gtg cgg cgc ggc gct gca gcc agc ctg			528
56	Gly Gly His Gln Leu Asp Val Arg Pro Arg Gly Ala Ala Ala Ser Leu			
57	165	170	175	
58	gct gac ttc qtg gag aac gtg gag tgg cgc gtg ctg ggc atg cct gct			576
59	Ala Asp Phe Val Glu Asn Val Glu Trp Arg Val Leu Gly Met Pro Ala			
60	180	185	190	
61	ccg ccg cgc gtg ctc acc tac ggc tgc tgc tcc gag ccc tac ccc gac			624
62	Arg Arg Arg Val Leu Thr Tyr Gly Cys Ser Glu Pro Tyr Pro Asp			
63	195	200	205	
64	gtc acc ttc acg ctg ctg cgc cgc ggc gcc tac gtg tgc			672
65	Val Thr Phe Thr Leu Leu Arg Arg Ala Ala Ala Tyr Val Cys			
66	210	215	220	
67	aac ctg ctg ccc tgc gtg ctc atc tcg ctg ctt gct ccc ctc gcc			720
68	Asn Leu Leu Pro Cys Val Leu Ile Ser Leu Leu Ala Pro Leu Ala			
69	225	230	235	240
70	ttc cac ctg cct gcc gac tca ggc gag aag gtg tcg ctg ggc gtc acc			768
71	Phe His Leu Pro Ala Asp Ser Gly Glu Lys Val Ser Leu Gly Val Thr			
72	245	250	255	
73	gtg ctg ctg gct ctc acc gtc ttc cag ttg ctg ctg gcc gag agc atg			816
74	Val Leu Leu Ala Leu Thr Val Phe Gln Leu Leu Leu Ala Glu Ser Met			
75	260	265	270	
76	cca ccg gcc gag agc gtg ccg ctc atc ggg aag tac tac atg gct act			864
77	Pro Pro Ala Glu Ser Val Pro Leu Ile Gly Lys Tyr Tyr Met Ala Thr			
78	275	280	285	
79	atg acc atg gtc aca ttc tca aca gca ctc acc atc ctt atc atg aac			912
80	Met Thr Met Val Thr Phe Ser Thr Ala Leu Thr Ile Leu Ile Met Asn			
81	290	295	300	
82	ctg cat tac tgt ggt ccc agt gtc cgc cca gtg cca gcc tgg gct agg			960
83	Leu His Tyr Cys Gly Pro Ser Val Arg Pro Val Pro Ala Trp Ala Arg			
84	305	310	315	320
85	gcc ctc ctg ctg gga cac ctg gca cgg ggc ctg tgc gtg cgg gaa aga			1008
86	Ala Leu Leu Leu Gly His Leu Ala Arg Gly Leu Cys Val Arg Glu Arg			
87	325	330	335	
88	ggg gag ccc tgt ggg cag tcc agg cca cct gag tta tct cct agc ccc			1056
89	Gly Glu Pro Cys Gly Gln Ser Arg Pro Pro Glu Leu Ser Pro Ser Pro			
90	340	345	350	
91	cag tcg cct gaa gga ggg gct ggc ccc cca gct ggc cct tgc cac gag			1104
92	Gln Ser Pro Glu Gly Gly Ala Gly Pro Pro Ala Gly Pro Cys His Glu			
93	355	360	365	

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94	cca cga tgt ctg tgc cgc cag gaa gcc cta ctg cac cac gta gcc acc	1152
95	Pro Arg Cys Leu Cys Arg Gln Glu Ala Leu Leu His His Val Ala Thr	
96	370 375 380	
97	att gcc aat acc ttc cgc agc cac cga gct gcc cag cgc tgc cat gag	1200
98	Ile Ala Asn Thr Phe Arg Ser His Arg Ala Ala Gln Arg Cys His Glu	
99	385 390 395 400	
100	gac tgg aag cgc ctg gcc cgt gtg atg gac cgc ttc ttc ctg gcc atc	1248
101	Asp Trp Lys Arg Leu Ala Arg Val Met Asp Arg Phe Phe Leu Ala Ile	
102	405 410 415	
103	ttc ttc tcc atg gcc ctg gtc atg agc ctc ctg gtg ctg gtg cag gcc	1296
104	Phe Phe Ser Met Ala Leu Val Met Ser Leu Leu Val Leu Val Gln Ala	
105	420 425 430	
106	ctg	1299
107	Leu	
109	<210> SEQ ID NO: 2	
110	<211> LENGTH: 433	
111	<212> TYPE: PRT	
112	<213> ORGANISM: Homo Sapiens	
113	<400> SEQUENCE: 2	
114	Val Glu Thr Glu Cys Leu Gly Ala Glu Gly Arg Leu Ala Leu Lys Leu	
115	1 5 10 15	
116	Phe Arg Asp Leu Phe Ala Asn Tyr Thr Ser Ala Leu Arg Pro Val Ala	
117	20 25 30	
118	Asp Thr Asp Gln Thr Leu Asn Val Thr Leu Glu Val Thr Leu Ser Gln	
119	35 40 45	
120	Ile Ile Asp Met Asp Glu Arg Asn Gln Val Leu Thr Leu Tyr Leu Trp	
121	50 55 60	
122	Ile Arg Gln Glu Trp Thr Asp Ala Tyr Leu Arg Trp Asp Pro Asn Ala	
123	65 70 75 80	
124	Tyr Gly Gly Leu Asp Ala Ile Arg Ile Pro Ser Ser Leu Val Trp Arg	
125	85 90 95	
126	Pro Asp Ile Val Leu Tyr Asn Lys Ala Asp Ala Gln Pro Pro Gly Ser	
127	100 105 110	
128	Ala Ser Thr Asn Val Val Leu Arg His Asp Gly Ala Val Arg Trp Asp	
129	115 120 125	
130	Ala Pro Ala Ile Thr Arg Ser Ser Cys Arg Val Asp Val Ala Ala Phe	
131	130 135 140	
132	Pro Phe Asp Ala Gln His Cys Gly Leu Thr Phe Gly Ser Trp Thr His	
133	145 150 155 160	
134	Gly Gly His Gln Leu Asp Val Arg Pro Arg Gly Ala Ala Ser Leu	
135	165 170 175	
136	Ala Asp Phe Val Glu Asn Val Glu Trp Arg Val Leu Gly Met Pro Ala	
137	180 185 190	
138	Arg Arg Arg Val Leu Thr Tyr Gly Cys Cys Ser Glu Pro Tyr Pro Asp	
139	195 200 205	
140	Val Thr Phe Thr Leu Leu Leu Arg Arg Ala Ala Ala Tyr Val Cys	
141	210 215 220	
142	Asn Leu Leu Leu Pro Cys Val Leu Ile Ser Leu Leu Ala Pro Leu Ala	
143	225 230 235 240	

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144 Phe His Leu Pro Ala Asp Ser Gly Glu Lys Val Ser Leu Gly Val Thr
 145 245 250 255
 146 Val Leu Leu Ala Leu Thr Val Phe Gln Leu Leu Leu Ala Glu Ser Met
 147 260 265 270
 148 Pro Pro Ala Glu Ser Val Pro Leu Ile Gly Lys Tyr Tyr Met Ala Thr
 149 275 280 285
 150 Met Thr Met Val Thr Phe Ser Thr Ala Leu Thr Ile Leu Ile Met Asn
 151 290 295 300
 152 Leu His Tyr Cys Gly Pro Ser Val Arg Pro Val Pro Ala Trp Ala Arg
 153 305 310 315 320
 154 Ala Leu Leu Leu Gly His Leu Ala Arg Gly Leu Cys Val Arg Glu Arg
 155 325 330 335
 156 Gly Glu Pro Cys Gly Gln Ser Arg Pro Pro Glu Leu Ser Pro Ser Pro
 157 340 345 350
 158 Gln Ser Pro Glu Gly Ala Gly Pro Pro Ala Gly Pro Cys His Glu
 159 355 360 365
 160 Pro Arg Cys Leu Cys Arg Gln Glu Ala Leu Leu His His Val Ala Thr
 161 370 375 380
 162 Ile Ala Asn Thr Phe Arg Ser His Arg Ala Ala Gln Arg Cys His Glu
 163 385 390 395 400
 164 Asp Trp Lys Arg Leu Ala Arg Val Met Asp Arg Phe Phe Leu Ala Ile
 165 405 410 415
 166 Phe Phe Ser Met Ala Leu Val Met Ser Leu Leu Val Leu Val Gln Ala
 167 420 425 430
 168 Leu

170 <210> SEQ ID NO: 3

171 <211> LENGTH: 1501

172 <212> TYPE: DNA

173 <213> ORGANISM: Homo sapiens

174 <220> FEATURE:

175 <221> NAME/KEY: CDS

176 <222> LOCATION: (34)..(1386)

177 <400> SEQUENCE: 3

178 gagacctgcc cccgcttgc cagtgccagg gcc atg ggg ctc cgg agc cac cac 54
 179 Met Gly Leu Arg Ser His His
 180 1 5
 181 ctc agc ctg ggc ctt ctg ctt ctg ttt cta ctc cct gca gag tgc ctg 102
 182 Leu Ser Leu Gly Leu Leu Leu Phe Leu Leu Pro Ala Glu Cys Leu
 183 10 15 20
 184 gga gct gag ggc cgg ctg gct ctc aag ctg ttc cgt gac ctc ttt gcc 150
 185 Gly Ala Glu Gly Arg Leu Ala Leu Lys Leu Phe Arg Asp Leu Phe Ala
 186 25 30 35
 187 aac tac aca agt gcc ctg aga cct gtg gca gac aca gac cag act ctg 198
 188 Asn Tyr Thr Ser Ala Leu Arg Pro Val Ala Asp Thr Asp Gln Thr Leu
 189 40 45 50 55
 190 aat gtg acc ctg gag gtg aca ctg tcc cag atc atc gac atg gat gaa 246
 191 Asn Val Thr Leu Glu Val Thr Leu Ser Gln Ile Ile Asp Met Asp Glu
 192 60 65 70
 193 cgg aac cag gtg acc ctg tat ctg tgg ata cgg cag gag tgg aca 294

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194	Arg Asn Gln Val Leu Thr Leu Tyr Leu Trp Ile Arg Gln Glu Trp Thr				
195	75	80	85		
196	gat gcc tac cta cga tgg gac ccc aat gcc tat ggt ggc ctg gat gcc			342	
197	Asp Ala Tyr Leu Arg Trp Asp Pro Asn Ala Tyr Gly Gly Leu Asp Ala				
198	90	95	100		
199	atc cgc atc ccc agc agt ctt gtg tgg cgg cca gac atc gta ctc tat			390	
200	Ile Arg Ile Pro Ser Ser Leu Val Trp Arg Pro Asp Ile Val Leu Tyr				
201	105	110	115		
202	aac aaa gcc gac gcg cag cct cca ggt tcc gcc agc acc aac gtg gtc			438	
203	Asn Lys Ala Asp Ala Gln Pro Pro Gly Ser Ala Ser Thr Asn Val Val				
204	120	125	130	135	
205	ctg cgc cac gat ggc gcc gtg cgc tgg gac gcg ccc gcc atc acg cgc			486	
206	Leu Arg His Asp Gly Ala Val Arg Trp Asp Ala Pro Ala Ile Thr Arg				
207	140	145	150		
208	agc tcg tgc cgc gtg gat gta gca gcc ttc ccg ttc gac gcc cag cac			534	
209	Ser Ser Cys Arg Val Asp Val Ala Ala Phe Pro Phe Asp Ala Gln His				
210	155	160	165		
211	tgc ggc ctg acg ttc ggc tcc tgg act cac ggc ggg cac caa ctg gat			582	
212	Cys Gly Leu Thr Phe Gly Ser Trp Thr His Gly Gly His Gln Leu Asp				
213	170	175	180		
214	gtg cgg ccg cgc ggc gct gca gcc agc ctg gcg gac ttc gtg gag aac			630	
215	Val Arg Pro Arg Gly Ala Ala Ser Leu Ala Asp Phe Val Glu Asn				
216	185	190	195		
217	gtg gag tgg cgc gtg ctg ggc atg ccg gcg cgg cgc gtg ctc acc			678	
218	Val Glu Trp Arg Val Leu Gly Met Pro Ala Arg Arg Arg Val Leu Thr				
219	200	205	210	215	
220	tac ggc tgc tgc tcc gag ccc tac ccc gac gtc acc ttc acg ctg ctg			726	
221	Tyr Gly Cys Cys Ser Glu Pro Tyr Pro Asp Val Thr Phe Thr Leu Leu				
222	220	225	230		
223	ctg cgc cgc gcc gcc tac gtg tgc aac ctg ctg ctg ccc tgc			774	
224	Leu Arg Arg Ala Ala Tyr Val Cys Asn Leu Leu Pro Cys				
225	235	240	245		
226	gtg ctc atc tcg ctg ctt gcg ccg ctc gcc ttc cac ctg cct gcc gac			822	
227	Val Leu Ile Ser Leu Ala Pro Leu Ala Phe His Leu Pro Ala Asp				
228	250	255	260		
229	tca ggc gag aag gtg tcg ctg ggc gtc acc gtg ctg ctg gcg ctc acc			870	
230	Ser Gly Glu Lys Val Ser Leu Gly Val Thr Val Leu Ala Leu Thr				
231	265	270	275		
232	gtc ttc cag ttg ctg ctg ggc gag agc atg cca ccg gcc gag agc gtg			918	
233	Val Phe Gln Leu Leu Ala Glu Ser Met Pro Pro Ala Glu Ser Val				
234	280	285	290	295	
235	ccg ctc atc ggg aag tac tac atg gcc act atg acc atg gtc aca ttc			966	
236	Pro Leu Ile Gly Lys Tyr Tyr Met Ala Thr Met Thr Met Val Thr Phe				
237	300	305	310		
238	tca aca gca ctc acc atc ctt atc atg aac ctg cat tac tgt ggt ccc			1014	
239	Ser Thr Ala Leu Thr Ile Leu Ile Met Asn Leu His Tyr Cys Gly Pro				
240	315	320	325		
241	agt gtc cgc cca gtg cca gcc tgg gct agg gcc ctc ctg ctg gga cac			1062	
242	Ser Val Arg Pro Val Pro Ala Trp Ala Arg Ala Leu Leu Gly His				

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/31/2004
PATENT APPLICATION: US/10/718,933 TIME: 12:19:12

Input Set : N:\CrF3\RULE60\10718933.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; Xaa Pos. 101

Seq#:20; Xaa Pos. 101

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/718,933

DATE: 08/31/2004

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Input Set : N:\Crf3\RULE60\10718933.raw

Output Set: N:\CRF4\08312004\J718933.raw

:689 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
:691 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
:718 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:19
:718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:751
:750 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19
:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:96